Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claim 1 (currently amended): A method for predicting one or more locations of single nucleotide polymorphisms, comprising the steps of:

obtaining a variation predictiveness matrix; and

predicting one or more locations of single nucleotide polymorphisms of a nucleic acid sequence based on the variation predictiveness matrix.

Claim 2 (original): The method of claim 1 further comprising one or more nucleic acid sequences with chemical modifications.

Claim 3 (original): The method of 2, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid sequence as a whole.

Claim 4 (original): The method of claim 1, wherein the step of predicting the likelihood of one or more single nucleotide polymorphisms comprises the steps of:

comparing the nucleic acid sequence one or more bases at a time with the variation predictiveness matrix to assign a variation value to bases in the nucleic acid sequence; and

selecting the polymorphisms that will likely cause a variation in one or more bases of the nucleic sequence based on the variation value.

Claim 5 (original): The method of claim 4, wherein the variation in one or more bases is nonsynonymous.

Claim 6 (original): The method of claim 4, wherein the variation in one or more bases is synonymous.

Claim 7 (original): The method of claim 1, further comprising the step of generating a dataset of single nucleotide polymorphisms for one or more nucleic acid sequences.

Claim 8 (original): The method as of claim 1, wherein the step of obtaining a variation predictiveness matrix, further comprises the steps of:

calculating a variation frequency from a first base to a second base in a dataset of two or more genes; and

generating the variation predictiveness matrix from the calculated variation frequency.

Claim 9 (original): The method of claim 8 wherein the dataset comprises genes with nucleic acid chemical modifications.

Claim 10 (original): The method of claim 9, wherein the chemical modifications include methylation or other chemical groups that incorporate additional charge, polarizability, hydrogen bonding, electrostatic interaction, and fluxionality to the individual nucleic acid bases or to the nucleic acid sequence as a whole.

Claim 11 (withdrawn)

Claim 12 (original): The method of claim 8, wherein the variation frequency is determined from a dataset of known diseases.

Claims 13-21 (withdrawn)

Claim 22 (currently amended): The method of claim 8, wherein the variation frequency is ~~further~~ adjusted for wild type genes.

Claims 23-36 (withdrawn)

Claim 37 (original): The method of claim 8, wherein the nucleic acid sequence comprises a cDNA sequence.

Claim 38 (original): The method of claim 8, wherein the nucleic acid sequence comprises genomic sequence.

Claim 39 (original): The method of claim 8, wherein the nucleic acid sequence comprises an intron/exon boundary.

Claim 40 (original): The method of claim 8, wherein the nucleic acid sequence comprises a transcriptional control sequence.

Claim 41 (original): The method of claim 8, wherein the nucleic acid sequence comprises a transport control sequence.

Claim 42 (original): The method of claim 8, wherein the nucleic acid sequence comprises a translational control sequence.

Claim 43 (cancelled)

Claim 44 (original): The method of claim 8, wherein the nucleic acid sequence comprises a splicing control sequence.

Claim 45 (original): The method of claim 1, wherein the step of obtaining a variation predictiveness matrix correlates the frequency of a first codon mutation to a second codon mutation with a variation predictiveness value of a nucleic acid sequence from one to ten bases at a time.

Claim 46 (original): The method of claim 1, wherein the variation predictiveness matrix is normalized for the codon usage of a target organism.

Claim 47 (original): The method of claim 1, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database.

Claim 48 (original): The method of claim 1, wherein the variation predictiveness matrix is generated from a mutant gene dataset that comprises all mutant genes in a mutant gene database minus the known mutant genes of the mutant gene dataset.

Claim 49 (original): The method of claim 1, wherein the nucleic acid sequence comprises an entire genome.

Claim 50 (original): The method of claim 1, wherein the nucleic acid sequence comprises a human genome.

Claim 51 (original): The method of claim 1, wherein the nucleic acid sequence comprises a gene cluster for a target human disease.

Claim 52 (original): The method of claim 1, wherein the variation predictiveness matrix is based on a mutant gene dataset that comprises a human mutation database.

Claim 53 (currently amended): The method of claim 1, wherein the steps are ~~affected~~ effected by a computer program.

Claim 54 (original): The method of claim 53, wherein the computer program is SNIDE.

Claim 55 (cancelled)

Claim 56 (original): The method of claim 1, wherein the variation predictiveness matrix is determined in silico from a human mutant database.

Claim 57 (original): The method of claim 1, wherein the step of predicting a likelihood of one or more single nucleotide polymorphisms is determined in silico.

Claim 58-202 (withdrawn)

Claim 203 (currently amended): A computer program embodied on a computer readable medium for predicting one or more locations of variations, comprising:

a code segment for creating variation predictiveness matrix from a nucleic acid dataset;

a code segment for comparing a wild-type gene sequence with the variation predictiveness matrix; and

a code segment for predicting one or more locations of variations in the wild-type gene sequence based on the comparison.

Claim 204 (currently amended): A computer program embodied on a computer readable medium for predicting one or more locations of polymorphisms, comprising:

a code segment for creating a codon mutation predictiveness matrix from a mutant gene dataset;

a code segment for comparing a wild-type gene sequence with the codon polymorphism predictiveness matrix; and

a code segment for ~~creating~~ predicting one or more locations of polymorphisms in the wild-type gene sequence based on the comparison.

Claims 205-213 (withdrawn)